

## Listing of Claims

The following listing of claims replaces all previous listings or versions thereof:

1-43. (Canceled)

44. (Currently amended) A method of assessing protein stability, folding and/or solubility comprising:

- a) ~~providing~~expressing in a host cell a fusion protein comprising (i) a protein of interest and (ii) a first segment of a marker protein, wherein said first segment ~~does not affect~~has only systemic effects on the stability, folding and/or solubility of the protein of interest;
- b) contacting said fusion protein produced in step a) with a second segment of said marker protein, wherein said second segment is capable of structural complementation with said first segment; and
- [[d]]c) determining structural complementation,

wherein a greater degree of structural complementation, as compared to structural complementation observed with appropriate negative controls, indicates stability, proper folding and/or solubility of said protein of interest.

45. (Previously presented) The method of claim 44, wherein said fusion is C-terminal to said protein of interest.

46. (Previously presented) The method of claim 44, wherein said fusion is N-terminal to said protein of interest.

47. (Previously presented) The method of claim 44, wherein said marker protein is selected from the group consisting of a target binding protein, an enzyme, a protein inhibitor, a fluorophore and a chromophore.

48. (Previously presented) The method of claim 47, wherein said marker protein is a target binding protein.
49. (Previously presented) The method of claim 48, wherein said target binding protein is ubiquitin.
50. (Previously presented) The method of claim 47, wherein said marker protein is a chromophore.
51. (Previously presented) The method of claim 50, wherein said chromophore is green fluorescent protein, blue fluorescent protein, yellow fluorescent protein, luciferase or aquorin.
52. (Previously presented) The method of claim 47, wherein said marker protein is an enzyme.
53. (Previously presented) The method of claim 52, wherein said enzyme is  $\beta$ -galactosidase, cytochrome c, chymotrypsin inhibitor, Rnase, phosphoglycerate kinase, invertase, staphylococcal nuclease, thioredoxin C, lactose permease, amino acyl tRNA synthase, and dihydrofolate reductase.
54. (Previously presented) The method of claim 53, wherein said enzyme is  $\beta$ -galactosidase.
55. (Previously presented) The method of claim 54, wherein said first segment is the  $\alpha$ -peptide of  $\beta$ -galactosidase, and said second segment is the  $\omega$ -peptide of  $\beta$ -galactosidase.
56. (Previously presented) The method of claim 44, wherein said protein of interest is Alzheimer's amyloid peptide ( $A\beta$ ), SOD1, presenillin 1 and 2,  $\alpha$ -synuclein, amyloid A, amyloid P, CFTR, transthyretin, amylin, lysozyme, gelsolin, p53, rhodopsin, insulin, insulin receptor, fibrillin,  $\alpha$ -ketoacid dehydrogenase, collagen, keratin, PRNP, immunoglobulin light chain, atrial natriuretic peptide, seminal vesicle exocrine protein,

β2-microglobulin, PrP, precalcitonin, ataxin 1, ataxin 2, ataxin 3, ataxin 6, ataxin 7, huntingtin, androgen receptor, CREB-binding protein, dentatorubral pallidoluysian atrophy-associated protein, maltose-binding protein, ABC transporter, glutathione S transferase, and thioredoxin.

57. (Previously presented) The method of claim 44, wherein said negative control utilizes a fusion protein that is improperly folded and/or insoluble.